



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/550,163B  
Source: 1FW/b  
Date Processed by STIC: 12/29/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

*Effective 12/13/03:* TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/550,1638

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>      Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n/Xaa      "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

## RAW SEQUENCE LISTING

DATE: 12/29/2003

PATENT APPLICATION: US/09/550,163B

TIME: 18:29:45

Input Set : A:\09550163b.txt

Output Set: N:\CRF4\12292003\I550163B.raw

3 <110> APPLICANT: University of Utah Research Foundation  
 4 Yale University  
 5 Abbott, Geoffrey W  
 6 Sesti, Federico  
 7 Splawski, Igor  
 8 Keating, Mark T  
 9 Goldstein, Steve A.N.  
 11 <120> TITLE OF INVENTION: MinK-Related Genes, Formation of Potassium Channels and  
 12 Association with Cardiac Arrhythmia  
 14 <130> FILE REFERENCE: 2323-150.a  
 16 <140> CURRENT APPLICATION NUMBER: 09/550,163B  
 17 <141> CURRENT FILING DATE: 2000-04-14  
 19 <150> PRIOR APPLICATION NUMBER: US 60/129,404  
 20 <151> PRIOR FILING DATE: 1999-04-15  
 22 <160> NUMBER OF SEQ ID NOS: 22  
 23 <170> SOFTWARE: PatentIn version 3.1/2.0

Does Not Comply  
 Corrected Diketite Needed  
 pp 1-3

## ERRORED SEQUENCES

774 <210> SEQ ID NO: 21  
 775 <211> LENGTH: 130  
 776 <212> TYPE: PRT  
 777 <213> ORGANISM: rattus norvegicus  
 E--> 779 <400> SEQUENCE: 321  
 781 Met Ala Leu Ser Asn Ser Thr Thr Val Leu Pro Phe Leu Ala Ser Leu  
 782 1 5 10 15  
 785 Trp Gln Glu Thr Asp Glu Pro Gly Gly Asn Met Ser Ala Asp Leu Ala  
 786 20 25 30  
 789 Arg Arg Ser Gln Leu Arg Asp Asp Ser Lys Leu Glu Ala Leu Tyr Ile  
 790 35 40 45  
 793 Leu Met Val Leu Gly Phe Phe Gly Phe Phe Thr Leu Gly Ile Met Leu  
 794 50 55 60  
 797 Ser Tyr Ile Arg Ser Lys Lys Leu Glu His Ser His Asp Pro Phe Asn  
 798 65 70 75 80  
 801 Val Tyr Ile Glu Ser Asp Ala Trp Gln Glu Lys Gly Lys Ala Leu Phe  
 802 85 90 95  
 805 Gln Ala Arg Val Leu Glu Ser Phe Arg Ala Cys Tyr Val Ile Glu Asn  
 806 100 105 110  
 809 Gln Ala Ala Val Glu Gln Pro Ala Thr His Leu Pro Glu Leu Lys Pro  
 810 115 120 125  
 813 Leu Ser  
 814 130

## RAW SEQUENCE LISTING

DATE: 12/29/2003

PATENT APPLICATION: US/09/550,163B

TIME: 18:29:45

Input Set : A:\09550163b.txt

Output Set: N:\CRF4\12292003\I550163B.raw

817 <210> SEQ ID NO: 22  
818 <211> LENGTH: 129  
819 <212> TYPE: PRT  
820 <213> ORGANISM: homo sapiens  
E--> 823 <400> SEQUENCE: ④22  
825 Met Ile Leu Ser Asn Thr Thr Ala Val Thr Pro Phe Leu Thr Lys Leu  
826 1 5 10 15  
829 Trp Gln Glu Thr Val Gln Gln Gly Gly Asn Met Ser Gly Leu Ala Arg  
830 20 25 30  
833 Arg Ser Pro Arg Ser Gly Asp Gly Lys Leu Glu Ala Leu Tyr Val Leu  
834 35 40 45  
837 Met Val Leu Gly Phe Phe Gly Phe Phe Thr Leu Gly Ile Met Leu Ser  
838 50 55 60  
841 Tyr Ile Arg Ser Lys Lys Leu Glu His Ser Asn Asp Pro Phe Asn Val  
842 65 70 75 80  
845 Tyr Ile Glu Ser Asp Ala Trp Gln Glu Lys Asp Lys Ala Tyr Val Gln  
846 85 90 95  
849 Ala Arg Val Leu Glu Ser Tyr Arg Ser Cys Tyr Val Val Glu Asn His  
850 100 105 110  
853 Leu Ala Ile Glu Gln Pro Asn Thr His Leu Pro Glu Thr Lys Pro Ser  
854 115 120 125  
857 Pro

see p. 3

09/550,163B

3

<210> 19  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HA residues for  
epitope mapping

<220>

<221> PEPTIDE

<222> (10)

<223> Xaa represents encoded stop codon.

*Xaa cannot represent a stop  
codon,*

<400> 19

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Xaa  
1 5 10

*Since a  
stop codon  
cannot  
encode an  
amino acid*

*same error in Sequence 20*

*(see item 13 on  
Error Summary  
sheet)*

**VERIFICATION SUMMARY**

DATE: 12/29/2003

PATENT APPLICATION: **US/09/550,163B**

TIME: 18:29:46

Input Set : **A:\09550163b.txt**

Output Set: **N:\CRF4\12292003\I550163B.raw**

L:751 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0

L:769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0

L:779 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:21 differs:3

L:823 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:22 differs:4